

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg Gly

20 25 30

Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu

35 40 45

5 Asn Tyr Cys Asn

50 55

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu

15 1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe

20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn

35 40 45

20 Pro Leu Gly Thr Gly Pro Arg Phe Val Asn Gln His Ile Cys Gly Ser

50 55 60

His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe

65 70 75 80

Tyr Thr Pro Lys Thr Arg Gly Ile Val Glu Gln Cys Cys Thr Ser Ile

25 85 90 95

Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

100 105 110

(8) INFORMATION FOR SEQ ID NO: 7:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

35 Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu

1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

5 Pro Gln Thr Ser Leu Ser Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Gly Thr Gly
10 85 90 95

Pro Arg Phe Val Asn Gln His Ile Cys Gly Ser His Leu Val Glu Ala
100 105 110

Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
115 120 125

15 Arg Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln
130 135 140

Leu Glu Asn Tyr Cys Asn
145 150

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CLAIMS**WHAT IS CLAIMED IS:**

1. A chimeric protein comprising, from N-terminus to C-terminus:
 - 5 a) a first peptidyl fragment consisting of an amino acid sequence that has at least 40% identity to a domain containing at least first 20 N-terminal amino acids of human growth hormone (hGH) protein, in which the percentage identity is determined over an amino acid sequence of identical size to the domain of hGH;
 - 10 b) an Arg residue, or a Lys residue, or a second peptidyl fragment consisting of at least 2 amino acids in which peptidyl fragment the most C-terminal amino acid residue is an Arg or a Lys residue; and
 - 15 c) a third peptidyl fragment consisting of an amino acid sequence containing more than two cysteine (Cys) residues which peptidyl fragment is not a portion of hGH protein.
- 20 2. The chimeric protein of claim 1, wherein the first peptidyl fragment consists of an amino acid sequence that has at least 60% identity to the domain of hGH protein.
- 25 3. The chimeric protein of claim 1, wherein the first peptidyl fragment is capable of being bound by an anti-hGH antibody.
4. The chimeric protein of claim 1, wherein the first peptidyl fragment 25 consists of the amino acid sequence of SEQ ID NO:1.
5. The chimeric protein of claim 1, wherein the first peptidyl fragment consists of the amino acid sequence of SEQ ID NO:2.
- 30 6. The chimeric protein of claim 1, wherein the second peptidyl fragment consists of the amino acid sequence of SEQ ID NO:3.
7. The chimeric protein of claim 1, wherein the third peptidyl fragment 35 is an insulin precursor.
8. The chimeric protein of claim 7, wherein the insulin precursor is of